

```

1 AATGGATTGG ACTCCGGTGG GGAAAGCGGG TGTCTAGAAG TGGTGCTAAT
51 GGAAGAGAGAA TTCTGGTTTC AAAAGAGGAT GCTCTGCCAC AAAGAGCGGC
101 TCGCGCGCTG GCCTGGGCTC TAGCCGAGGA GAGATCCCGG GAGAACTCCA
151 GAGCTCCGGG GGAGCGCTCC TCGGAAGACC GGGGCCAACA TGCCTGTGCG
201 CAGGGGGCAT GTGGCACCAC AAAATACATT TCTGGGGACC ATCATTCGGA
251 AATTGAAGG GCAAAATAAA AAATTTATCA TTGCAAATGC CAGAGTGCAG
301 AACTGTGCCA TCATTTATTG CAACGATGGG TTCTGTGAGA TGA CTGTTT
351 CTCCAGGCCA GATGTCATGC AAAAGCCATG CACCTGCGAC TTTCTCCATG
401 GACCCGAGAC CAAGAGGCAT GATATTGCCC AAATTGCCCC GGCATGCTG
451 GGGTCAGAAG AGAGGAAAGT GGAGGTCACC TACTATCACA AAAATGGGTC
501 CACTTTTATT TGTAACACTC ACATAATTCC AGTGAAAAAC CAAGAGGGCG
551 TGGCTATGAT GTTCATCATT AATTTTGAAT ATGTGACGGA TAATGAAAAAC
601 GCTGCCACCC CAGAGAGGGT AAACCCAATA TTACCAATCA AAAGTGTAAA
651 CCGGAAATTT TTTGGGTTC AATTCCCTGG TCTGAGACTT CTCACTTACA
701 GAAAGCAGTC CTTACCACAA GAAGACCCCG ATGTGGTGGT CATCGATTCA
751 TCTAAACACA GTGATGATTC AGTAGCCATG AAGCATTTTA AGTCTCCTAC
801 AAAAGAAAGC TGCAGCCCCCT CTGAAGCAGA TGACACAAAA GCTTTGATAC
851 AGCCCAGCAA ATGTTCTCCC TTGGTGAATA TATCCGGACC TCTTGACCAT
901 TCCTCTCCCA AAAGGCAATG GGACCGACTC TACCCTGACA TGCTGCAGTC
951 AAGTTCCOCAG CTGTCCCAT TCCAGATCAAG GGAAAGCTTA TGTA GTATAC
1001 GGAGAGCATC TTCGGTCCAT GATATAGAAG GATTGCGCGT CCACCCCAAG
1051 AACATATTTA GAGACCGACA TGCCAGCGAA GACAATGGTC GCAATGTCAA
1101 AGTTTCACGT TCCTGGATGG CAGGGGGGCC TTTTAATCAT ATCAAGTCAA
1151 GCCTCCTGGG ATCCACATCA GATTCAAACC TCAACAAATA CAGCACCATT
1201 AACAGATTTC CACAGCTCAC TCTGAATTTT TCAGAGGTCA AAAGTGAGAA
1251 AAAGAATTCA TCACCTCCTT CTTAGATAA AACCATTATT GCACCCAAGG
1301 TTAAAGATCG AACACACAAT GTGACTGAGA AAGTGACCCA GGTCTCTCT
1351 TTAGGAGCAG ATGTCCTACC TGAATACAAA CTGCAGACAC CACGCATCAA
1401 CAAGTTTACG ATATTGCACT ACAGCCCTTT CAAGGCAGTC TGGGACTGGC
1451 TTATCCTGCT GTTGGTCATA TACACTGCTA TATTTACTCC CTACTCTGCA
1501 GCCTTCTCTC TCAATGACAG AGAAGAACAG AAAAGACGAG AATGTGGCTA
1551 TTCTTGTAGC CCTTTGAATG TGGTAGACTT GATTGTGGAT ATTATGTTTA
1601 TCATAGATAT TTTAATAAAC TTCAGAACAA CATATGTAAA TCAGAATGAA
1651 GAAGTGGTAA GTGATCCCGC CAAAATAGCA ATACACTACT TCAAAGGCTG
1701 GTTCCTGATT GACATGGTTG CAGCAATTCC TTTTGA CTGATT TTTG
1751 GATCAGGTTT TGATGAGGTA AGAAGTCTT AAGATTCTTA TTTTCTGAAA
1801 GATTGCAATT ATAAAGTGA ATCTATTTTA ACTGCAAAAA GAAGAGTTGC
1851 TTTGCAAGCT TCTTGATCT CACTGATAAA ATTCATTTTC AATTGGGGAT
1901 ACTACAGAAT GAAATGAAAC CATTTTGCCA TTGCAAATCA AATTCTTTCT
1951 CTTTTTGCTA AGAGATGCAA AAGATTCTCC ATTCTTTACC CACCAAATTA
2001 AACTTGGAAG CAAGTGGTCC ATAGCACACA GCACATTCCC AGGATTTAAA
2051 ATCTCTACTT ATTAACCTCA CGGGTGTAAG ACTCTCAAAT ATTAAGTATG
2101 TCTCTGTTTT TCTTAACTCA TTGTTAAGGG TTTGAGACAG CAGAGATTG
2151 GTTTTTTTGT TCAAATTATT GTGAAGAGGG CCCCTTTTCC GAAAT (SEQ ID NO:1)

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FEATURES:

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5'UTR:      1-189
Start Codon: 190
Stop Codon:  1780
3'UTR:      1783

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HOMOLOGOUS PROTEINS:

Top 10 BLAST Hits:

	Score	E
CRA 113000007753533 /altid=gi 4104136 /def=gb AAD01946.1 (AF03...	1058	0.0
CRA 36000087530063 /altid=gi 11121258 /def=emb CAC14797.1 (AJ2...	1041	0.0
CRA 18000005124020 /altid=gi 2745727 /def=gb AAB94741.1 (AF016...	1039	0.0
CRA 18000005107889 /altid=gi 7305203 /def=ref NP_038597.1 pota...	592	e-168
CRA 18000005107891 /altid=gi 2582015 /def=gb AAC53420.1 (AF012...	591	e-168
CRA 18000005084931 /altid=gi 2190505 /def=emb CAB09536.1 (Z961...	589	e-167
CRA 18000004922641 /altid=gi 4557729 /def=ref NP_000229.1 pota...	580	e-164
CRA 108000024648805 /altid=gi 12733048 /def=ref XP_004743.2 po...	580	e-164
CRA 164000136746223 /altid=gi 11933152 /def=dbj BAB19682.1 (AB...	580	e-164
CRA 1000737074349 /altid=gi 6687230 /def=emb CAB64868.1 (AJ243...	570	e-161

BLAST dbEST hit:

gi 2229460 /dataset=dbest /taxon=9606 ...	434	e-119
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EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hit:

gi|2229460 testis

From tissue screening panels:

whole_brain

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1  MPVRRGHVAP QNTFLGTIIR KFEGQNKKEI IANARVQNC A IIYCNDGFCE
51 MTGFSRPDVM QKPCTCDFLH GPETKRHDIA QIAQALLGSE ERKVEVTTYH
101 KNGSTFICNT HIIPVKNQEG VAMMFLINFE YVTDNENAAT PERVNPILPI
151 KTVNRKFFGF KFPGLRLTY RKQSLPQEDP DVVVIDSSKH SDDSVAMKHF
201 KSPTKESCSF SEADDTKALI QPSKCSPLVN ISGPLDHSSP KRQWDRLYPD
251 MLQSSSQLSH SRSRESLCSI RRASSVHDIE GFGVHPKNIF RDRHASEDNG
301 RNVKVSRSWM AGGPFNHIKS SLLGSTSDSN LNKYSTINKI PQLTLNFSEV
351 KTEKKNSSPP SSDKTIIAPK VKDRTHNVTE KVTQVLSLGA DVLPEYKLQT
401 PRINKFTILH YSPFKAVWDW LILLLLVIYA IFTPYSA AFL LNDREEQKRR
451 ECGYSCSPLN VVDLIVDIMF IIDILINERT TYVNQNEEVV SDPAKIAIHY
501 FKGWFLIDMV AAIPFDLLIF GSGSDEVRTA (SEQ ID NO:2)

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FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION

N-glycosylation site

Number of matches: 4

1	102-105	NGST
2	230-233	NISG
3	346-349	NFSE
4	377-380	NVTE

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE

CAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 3

1	171-174	RKQS
2	271-274	RRAS
3	354-357	KKNS

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 9

1	74-76	TKR
2	169-171	TYR
3	187-189	SSK
4	239-241	SPK
5	269-271	SIR
6	352-354	TEK
7	379-381	TEK
8	362-364	SDK
9	352-354	TEK

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE

Casein kinase II phosphorylation site

Number of matches: 7

1	55-58	SRPD
2	133-136	TDNE
3	209-212	SPSE
4	211-214	SEAD
5	275-278	SVHD
6	325-328	STSD
7	522-525	SGSD

[5] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

Number of matches: 3

1 92-99 RKVEVTTY
2 241-248 KRQWDRLY
3 448-454 KRRECGY

[6] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

312-317 GGPFNH

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	420	440	1.885	Certain
2	504	524	1.071	Certain

BLAST Alignment to Top Hit:

```
>CRA|113000007753533 /altid=gi|4104136 /def=gb|AAD01946.1|
(AF032897) potassium channel subunit [Homo sapiens]
/org=Homo sapiens /taxon=9606 /dataset=nraa /length=1196
Length = 1196
```

Score = 1058 bits (2705), Expect = 0.0
Identities = 518/529 (97%), Positives = 519/529 (97%), Gaps = 8/529 (1%)

```
Query: 1  MPVRRGHVAPQNTFLGTIIRKFEGQNKKFIIANARVQNCAIYCNDGFCEMTGFSRDPVM 60
          MPVRRGHVAPQNTFLGTIIRKFEGQNKKFIIANARVQNCAIYCNDGFCEMTGFSRDPVM
Sbjct: 1  MPVRRGHVAPQNTFLGTIIRKFEGQNKKFIIANARVQNCAIYCNDGFCEMTGFSRDPVM 60

Query: 61  QKPCTCDFLHGPETKRHDIAQIAQALLGSEERKVEVTTYHKNKGSTFICNTHIIPVKNQEG 120
          QKPCTCDFLHGPETKRHDIAQIAQALLGSEERKVEVTTYHKNKGSTFICNTHIIPVKNQEG
Sbjct: 61  QKPCTCDFLHGPETKRHDIAQIAQALLGSEERKVEVTTYHKNKGSTFICNTHIIPVKNQEG 120

Query: 121 VAMMFIINFEYVTDNENAATPERVNPILPIKTVNRKFFGFKFGLRLLTYRKQSLPQEDP 180
          VAMMFIINFEYVTDNENAATPERVNPILPIKTVNRKFFGFKFGLR+LTYRKQSLPQEDP
Sbjct: 121 VAMMFIINFEYVTDNENAATPERVNPILPIKTVNRKFFGFKFGLRVLTYRKQSLPQEDP 180

Query: 181 DVVVIDSSKHSDDSVAMKHFKSPTKESCSPSEADDTKALIQPSKCSPLVNISGPLDHSSP 240
          DVVVIDSSKHSDDSVAMKHFKSPTKESCSPSEADDTKALIQPSKCSPLVNISGPLDHSSP
Sbjct: 181 DVVVIDSSKHSDDSVAMKHFKSPTKESCSPSEADDTKALIQPSKCSPLVNISGPLDHSSP 240

Query: 241 KRQWDRLYPDMLQSSSQLSHSRRESLCSIRRASSVHDIEGFGVHPKNI FRDRHASEDNG 300
          KRQWDRLYPDMLQSSSQLSHSRRESLCSIRRASSVHDIEGFGVHPKNI FRDRHASEDNG
Sbjct: 241 KRQWDRLYPDMLQSSSQLSHSRRESLCSIRRASSVHDIEGFGVHPKNI FRDRHASEDNG 300

Query: 301 RNVKVSRSWMAGGPFNHKSSLLGSTSDSNLNKYSTINKIPQLTLNFSEVKTEKKNSSPP 360
          RNVK          GPFNHKSSLLGSTSDSNLNKYSTINKIPQLTLNFSEVKTEKKNSSPP
Sbjct: 301 RNVK-----GPFNHKSSLLGSTSDSNLNKYSTINKIPQLTLNFSEVKTEKKNSSPP 352

Query: 361 SSDKTIIAPKVKDRTHNVTEKVTQVLSLGADVLPEYKLQTPRINKFTILHYSFPKAVWDW 420
          SSDKTIIAPKVKDRTHNVTEKVTQVLSLGADVLPEYKLQTPRINKFTILHYSFPKAVWDW
Sbjct: 353 SSDKTIIAPKVKDRTHNVTEKVTQVLSLGADVLPEYKLQTPRINKFTILHYSFPKAVWDW 412

Query: 421 LILLVVIYTAIFTTPYSAAFLNDREEQKRRECGYSCSPLNVVDLIVDIMFIIDILINFRT 480
          LILLVVIYTAIFTTPYSAAFLNDREEQKRRECGYSCSPLNVVDLIVDIMFIIDILINFRT
Sbjct: 413 LILLVVIYTAIFTTPYSAAFLNDREEQKRRECGYSCSPLNVVDLIVDIMFIIDILINFRT 472

Query: 481 TYVNQNEEVVSDPAKIAIH YFKGWFLIDMVA AIPFDLLIFGSGSDEVRT 529
          TYVNQNEEVVSDPAKIAIH YFKGWFLIDMVA AIPFDLLIFGSGSDE T
Sbjct: 473 TYVNQNEEVVSDPAKIAIH YFKGWFLIDMVA AIPFDLLIFGSGSDETTT 521 (SEQ ID NO:4)
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Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00914	Transmembrane region cyclic Nucleotide Gated	34.2	1.4e-08	1
CE00367	E00367 brain_cyclic_nucleotide_gated_channel	30.3	5.1e-08	1
PF00785	PAC motif	16.2	0.006	1
PF00989	PAS domain	6.4	3.7	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00989	1/1	41	60 ..	26	45 ..	6.4	3.7
PF00785	1/1	93	120 ..	1	28 [.	16.2	0.006
CE00367	1/1	467	516 ..	92	142 ..	30.3	5.1e-08
PF00914	1/1	500	526 ..	1	28 [.	34.2	1.4e-08